

FIG. 1

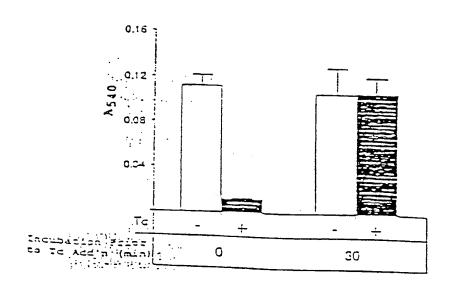


FIG. 2

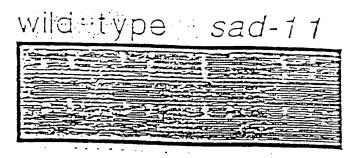


FIG. 3

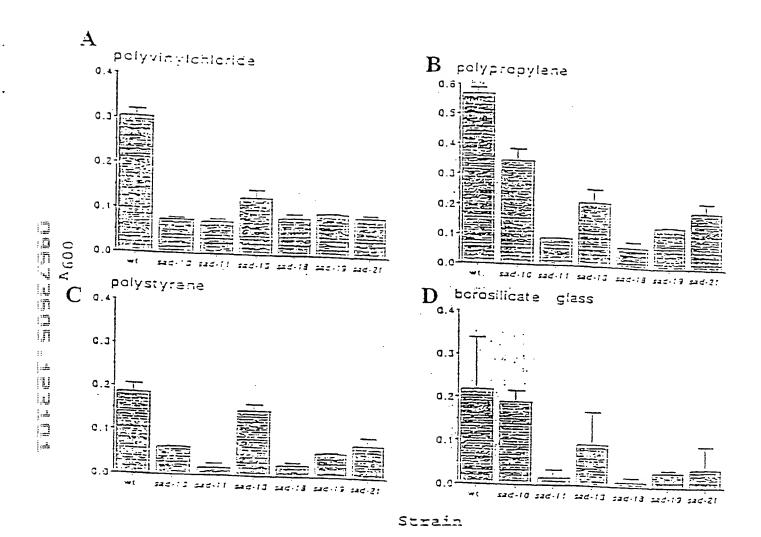


Fig. 4

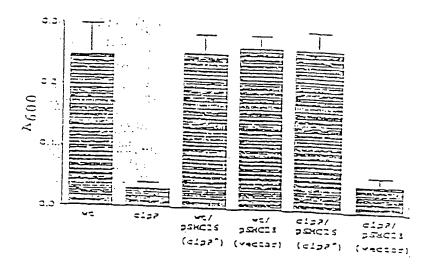


Fig. 5

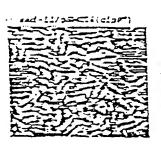




Fig. 6

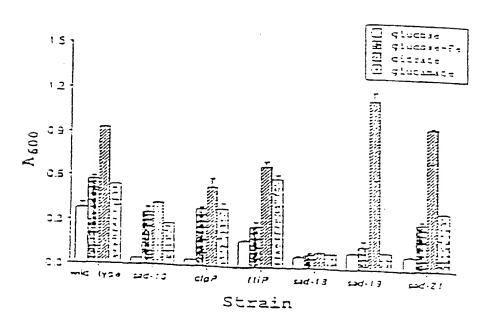


Fig. 7

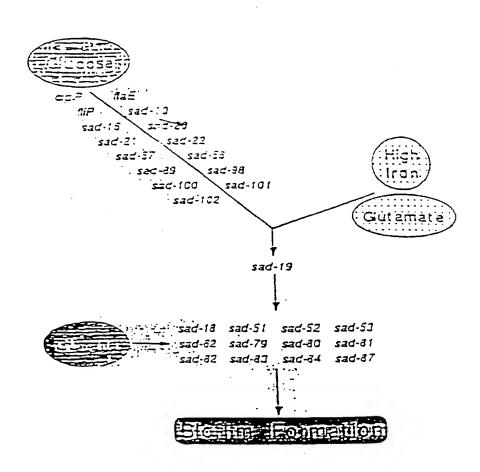


Fig. 8

540-13 SEQ ID NO: 4

GATGGE

sad-19 SEQ ID NO: 5

CNCAANGGONCAGAGCACAGGATATGONGCAATGTCATGGACAAACGGCGCCAGCCCNATGGAG GCCACCGACNCCACATCCGTCGCCGCCGGTTGCAGGCNCGCCAACGCANCCTCAAGGTTCTG CGCCANTTGCANCNCT CCTCGCNCACCANCONNAGTTGCCAGCNCCNCAAACTCCCCACCNCNA ANNONCHTNACNAAAT INTEGETTICEGNATACCECCNICACTEACECACCAATTECTCACCONC GGCCTG+ACN4ACTGGTCGGTN-CNCTNCCCGCCCCATCCNCTGGTTNAAACNGGCCNATTCCTN ACCCCAGCAACANCN. AATAACCCCGACCTGGCCANCNCCGGGTNGCTCACCCGGGCATTAAACC TGCATTTTCAAAATATNN.CCGGTTGGCCACGCCCGTNAGGTTGTCCTGNTAGGATCCNACCCCCA NTTTCNCTNTGCCCCT: GGNCTGNTCNNGGAANNGNNCCNTGAGCTTTCTCGACCATCTGGGTTTC TINCTENTGENECACTONEGN. NEAAGTITTAAGGTNTTNNETEEGGGNAATEETENNEGENA NININCTTNAACTGNAAACTTECNCCGAACNGGGNCCTAANANTAGNCCTATNINGGGGNNACNINGCG TECCAGOOGOGGGGTNTTCAAGTCNTTGAACGNAACTECT CNAGTONTTCCACANGGNCTCCCCCCTANTNTNTAACCGCGTNTCNTCTATNTTGGGNGTCCCCGN NTNCATACATGNCNGAGTANAA BAAGGTCNANCCTCCCNANNNGGNTCTCCGCCCCCAATTTNT CCCCTCTCTCCCTTTNANCNTCTAAATATATTCTTTNNTGGGNNTNAANAAGGGGGGGCGCANAAA NACCTNTCTCCGGGGGGGGTTGTGGGNCCTNNANAAACCCCCCTTTCTNTTNTNNNCCCCCCTCCG NGGGGGCTCCNCCCTCCCTNTTTGTTTTCCCCNCCTANNAATCCCTACTCNCNGGNCTAGTTG+A .4

Fig. 9

sed-21 SEQ ID NO: 7

>sad-10 SEQ ID NO: 1

GACCGCACNIAGAGGILACNGNCCGACGACGANCAGGACGACGACNAGNGGNAG GGANNNGGGNGGGGNNNTGNTTATNATNANGCTCCCCCCCGGACGAA GAAATTCCCGATGCATTGCTCGAGCGCGTAGGCCTGTCTCGGGACAAGGTCA ACCACGTATTCAGCAAAGTGCTCNAGGCGGAANTGCTGCTGCGCGAACTGCC CTCGCANTTC \GCC\CGGCTG\ATAGGCTCGCCCGGTCATTTGATCTTTCCCAC CCTCTCCGTGGGALATGEATCCCCTGACGCTCTGCGTCACATCTCAGAAGCGGA ACCCGGAGCGTCCCTCGCCACNTTCCCNCNCAGCGAGCGTCGGGAACCNANCA AACNTGGTCCCCTCG ATINTAAAGTTCTTCCTTAAAANCTTCTTNCGGGCTT CCAGGGTATILIGGTCCANCCCCCTTGGGAACCCANATCCCCCAGGGGGCCCCGG CGTTGCCCCC\.TTGATCCTGGGGATTCCGACTTTGTTCCTTGN.A.A.ATCCCCCCT TCCATTGALALCONCCCANGTTINGCCTTTTGTTTCCCTTTCGGCCCCNTNCCAA NTGTTACTNALNTNCANAACGCCNNTTGGGGCCANAAANNTCGNCTNGNGN NANNACANCENCATOTTINCTNCCCNTCCNNNCTNTNNTCCTCNGTGTATNTC CAANTONTSCOMOCCOMICOGCCTCCCCACINCCINSGCCCTCONNOCN CGOGTINCATENCTCCNOCNINNICCGCTINICCCCNTITANCGTNGCCGTINC CCCCCCGNINICINATIONNIGNOGCICTICCNCCCCIGTCCNCCCANT GCCNNCNNCTCCGAGGTCGCNGGTCTCNCCNCCNGNTTCGTOCNCNGGCN CNNGATCCCCTTCNCNCCNCNCNTNATCCTGACCAGINNGNGNGNGNCTNCNN NCCICCOGICNENACNIGININGNOGGGGGGCCCNCCC

>sad-11 Match: clipP SEQ ID NO: 2
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NANATCTACTCNCGTCTGCTCAANGAACGCGTCATCTTTCTGGTGGGCCCGGT
AAAAGACTACATGGCCNACCTGATCTGTGCGCAACINTTGTTCCTTGAANCC
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>sad-16 SEQ ID NO: 3

>sad-20 SEQ ID NO: 6

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>sad-22 SEQ ID NO: 8

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>sad-51 SEQ ID NO: 9

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GTCGTTTACACGCGCCCCGGTTAACCCACCCGTGACCGACGCTTCCGTTGGTTATC
ACCCTGTTCC VACCGCCANACCATCACCATCCGGTTGGNGCCAGCANCNGC
ACCGTGAAGATTGATG.ACGCCAAACGACGCCCTCGCGGGCGGCGATAACCTGAG
CGTGAAGATTGATG.ACGCCAAGGGTGGCAATTACNAAAAAACTTGGACATCG
ACCCTGACCCCGGCGCGACACCACCACCGGTTACCGGATNTGCAGGACACTACCGGCCTG
ACCTTGANTGCAACCGATAGCGTTGCTGAANGCGGNTCGATCGTTTACACCG
CAACATTGACCCAACGGCNCCGGNTCGCTGTAACCCTGAACCAACCG
NGCCGGTGATCAACCGCNCCCGGNTCGCCTGTAACCACCGG
NGCCGGTGATCAACATCCCTGCGGGGNGTTTCCCCCCCCGGTNCTANTCTACACGNG

>sad-52 SEQ ID NO: 10

>526-53 SEQ ID NO: 11

CTGGGTGT.4.T.4.4.C.4.TC.4.GGGCCCANTNGTGTCCTGG.AGTGTCTGT.V.AC.4.GTGG TTTCGGC4NGCTTGCCCTCNANATNCANTTTTTCGTAATTGCCACCCTATGGC CINCICO ALATTIGALANCACNAGNNACCINCCCANTONCALAGGGGCTICTICN GCVLCVVGVTTLC+VCCVACVVVVVTVCGGGCC44CCCLGFVLGGILTCC GICNICCCCO/CIC/CC/CATTICTCTCCCC/AACC/TCCCCGGI/CCI/CA/ TIGCCTICT.4.4CCC.4.4GCGNCNGNININNANCNCCITGTITCNCCCCTNCNG NCCNACGCGTCGA LAGGTTTIACCCCCATAGGGGGCTCNATTATTCTALLA CGCTTTTCC4.3.4.4.4.1.GGCCTGCCCGGTNT.4CVCCTTCTTAN.NINTCGTCCCG TCCNAGNGCTTATCNCTCTCTNNCCCCCTTCGGATACTNCTCTGTAAGTTTCCCT AAAATCVNCTGGNTVGGNTTCTNNCNANAAAGAANATCTNTGGGGGCCTTT NTNTNTTATATCCTCTCNTATIGTNCTTTNCNNTANCNTCTNTCCNNGANNC TCATICCCC ANACCCTCINNNNCCCCCCTTNCNCTCICNTATANTTICTNAGT TGAACCGCTCNTCCCCNCTNCACINITIATINNNTNNGCGGGNCGCNCNCTTGT COCTONTILA ACCOTOGOCONTNOCOGAGONTA ON GOCTONO I COCTA A INCTICTO GGCGGTNNNGGGGGCGNACGTCCTCGCCTTCGTTCNNAAATNNTTCNTAANTT CCAACNTCENGCNGCCCCGCTCCCGCNNNNNCAATNTINTCTCCCCCCCTATTCT NGCTACNCAGCGNGTGATNATCCCNTTCTCANNAGCCINTTCNGGGTATAAC NGNGNAGNGANNCTCTCTCTTTAGTNCONAANCOVATCTCTNCTCCTCTTC TTCNGGTCGCGCINCTANANCNCTGGTCAGTENNTCCTCNATGNNNCVNAG. GNTCCCNNTINCTCNCTCNCTTCTTGNNNACTCCCNGTNTGTCCNGGANTGGN TCTTCCGCCTCGGNANCNNTGCTCCTNTNTTCNCNANNCGAANANTCTCCTTN CTAACACNCCTTCGCCNAANACNTTITNACTCTNCCCTCNTCCTTCNCTNNCT CGTCTNATTNINANTINCNTNCCTANNCNGTGACTCGTTAGCNCTCCGNTCT TICOVANTCTTCGCCCCCCNTCTCOVCNCTCNANNCTATCCC

>sad-57 SEQ ID NO: 12



SEQ ID NO: 13

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>sad-62 SEQ ID NO: 14

GIGCTIGTGTATAAGNTCAGNCCCTGGCCTGNGCCCNCNACAACTCCCGGTNNCC GTCTACANTITAGCNAAGGATCGGTCATTGCCTNGTCTNCTGGNTANACTNC CGGGACNATCCACCTCAATACTCCNNCCATTNACGTCTATGGTAACCNGGAG GTCGGTCANCAGNNCNATTACCGGTNCTACCNGTGGAAACTTCGAAAATCT NGTGGCNAACACGGGACCTGCGGTCCCCNCCANTTCCGATTCNGGNGANACN NCATGGNTGTCNCNNACNGGNNGCNACNCCATTCCTGNANGGGNGCCAANTT CCTTICNICNTCAANCCGTNGGNAACGGGCCCNAATNCCGTNAACGTTACCNN NGANAAATGGTCNGTTTTCCATTCCCCCGGGGGNANAAACCGGGACNGAAG ATTTCAANACCCGCGCVTNTNATINTACCNNGGGGVNNGCGGCGTCGNCCCCCC NCNNNACNNGTGANAANGGGGGGCTNTTCAAANTTCNTNGTGTTNANCAC NACCCTGGCGTTTNATANTANTINCANAATTNCGGGNGGAANACCACCGGG CCTTNANNNCTTNNAACNGGNONNNCNACCNNCTTTCCNNNNNGGGGGGGG GTTCCNNCNNCCCCCCCNTINNNTINNTITNNAAANNTTTTTGGGGGAAAAA

>sad-79 SEQ ID NO: 15

TGCTTGTGT.4.T.4.4.G.4.TC4CGCCCCGNCGCCNCCCNNLNTTANGTCTGCGTC4.4 CGACACNNCATNGCTGCNGTGGNANCTCANTITACNAGGCNCTTAAAANGC ATNATIGET LENCACENGOCGAGGINGNECCTCCCNTANCCGAAGNNAIN TOWNACTICGALAN CATTINANCNITITCCANTCGGTNGNTACCAGNNGTG ANTONTOLANTITICTOLACACCONCTGGTNNCNNTCCTGTTCACNCCTANANNN GACCICTCTCCCCNTCNGGGCCTGGNCCNTAATATNNTACCGGCTTINNAN TGCTGTCAGTATNANTCTCCNNAGCNGNAAANTCNCTCTNCANNCGGTGTY THENGTOTONICTE STOCINCTONTACACTCACINACTINENCTONNALTO NATOTANICTOTANIATCACGONCANCNOGTICINTOTOGGGGCTCNOTTGANA GGCTCCCCCTNACCTCTCTANNACNGTGTCGGGTATNNCNCTATAANAGTC TTGTGCATGTNTCAC+GTN/ACATCGTCGCCN/NCNCGNGTACCTCTGCATCNT CGCCCTTTN.TTCTNTTCTCTCXCCAAANATCTTNNTNTCTCTCNNTCNATC ATTATTONCANGEGG: CTCCNTCCCCCTCNNNCNTCNGTTCNANAC ANGTONTATTI'AGCTATGTCTTATGTNCNCCTNTCANTTTINCTNCNCTTCN CACNCTTCACANNOGCTNNGNCTGACCTCTATAGTCGNTCNTCTCCTCCTCT NCINNTCTCTCNGCNATAACGCNCNINCNCTTCTGGNCTCTCNNGCTCTCTNN TMNTATATCCNNCGCCNNTTCTCTCTCTCTCTCTCCCCNTNTGTGCTCNTCAATTG TNONCTOTOGONONCTGTONNNTCTANCGTNT: CITGACTTNANNAATA CYTACCTCTCTNGCCTCTCINCNTNTNCTCTCNCCGCATCTCTNNGACCGCIN CCTCTGCNCNGCGCNATCTCTTCTTTNCGTTCTCCCNNTTCTCGCGNCTCTCTNNG TACINGCTTUTCCCNCTACCTNTCTCTTGCTCCTCGCNTCNTCINCCTCTC TCTTCTCTNTCTANGTCNNCNCGNCCATNGGCTTTCTCTCGCTNCNTNTCNCTC TICINICININCCGICICGICINGATCNNICICICATCATATNCININTINIC ATCANGCININTGNC+CICICCNATCIGINTCICINTCTTANTNNICCNICCT TCCINTICICITANCICNCGINNATINICNITICTCIGAINTCCTCNAGTAINTC TATGTACGCTNNCNTINATCCNGNNCCTNTCTCTATCANCATCATNCTAGCT MNCTTCCTATNGTCGIGCTCTCACTNTTTCTGCCNANATATNNATCNCTNCTC TNTATCTTCNTANATTNNINCCINTNAATGTTINANAATGCTCTACICNAN CTCTCTNTNTCTTNNNCTCCAGNTCACTCTCTANANNTGCCTNNCGTTATACG NTCTINTNCGCTTTANTGCGTNTNCTATCANTNNCGCTCTTTNTTCTCNTCT CNCCNTGTNCTTNNCACACINTCTTCATCICTTCICNNATATNNATGTCNNT CTATNINCONCTRUTATE CONTOUCCENTENANCE ACANTINENATORC

C8-prs< SEQ ID NO: 16

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>sad-81 SEQ ID NO: 17

ATNINGNINNTINCTTGTGTATAAGNTCAGGGCNCCNCCTNTCNNAACTTNG TCTGGGTCGNCCTACACNNCANNGGNNACTGGCAGCTCGGTNACCGCTACCTN ANAACGCTTCANTGTTCCTCAGCNGGTCCACGTCCAGCCTTGAGCCACATGIN AAAANNONGCONACAANCONNGONGTNAANNTCCACGNNNTGCNCGACGA NTGCCAATNNAANNTICTCNACNGITTCACCTGGAANGACCTTGCCGANAC CNANACNINTCACCAANGGTGAANNCAACTCCCGGNAGATNCGCTNCACNCC NGACCCCAACGAATCCTNCGCCGNNGGTTTTNTTAGCANCATCGNCGNCANC AACCANGNCCANTICNCCCCGNTNICATTCCNNCCNANCGACGGNNNNTCTG GGCGTCNCCCCCCCCGTACTANTCTACNCNINNCAAAAA

>sad-89 SEQ ID NO: 20

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>sad-83 SEQ ID NO: 18 19/34

>5ad-87 SEQ ID NO: 19

>sad-98 SEQ ID NO: 21

>sad-100 SEQ ID NO: 22

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>sad-101 SEQ ID NO: 23

TCTTTAANTAGNACCGACGANTCCTCCTANCACCCCTAACCAGTCNACGGCT NGTGGCGACTCGATATNGACACTNGACCAGGTCGGGGGCNTCNCCCCCACNNT NCTATTCAACGCTTGGCCAAACACGTGGTCANATCTCTCNCCAGTGCCCCTCN TANCNTTCTCCGATACACTINTCTTCTTCCAATATCCCCCGCTAATCCCCCTCTC ATCNGTGALNNGGCCCCCCCCTCCATTAAAAAGCAINGNGCNNACAAACAAC CNGAGATCNTTCNNNTTNNCANNCCTCCCGNTCCCTCAAATTTCGNNAGGGG NCCGGTTGCGACCCNAAACCGCNTCCNNGNGGNAAATTTCTTNCNTT

>sad-102 SEQ ID NO: 24

TNCTTGTGTATAAGNTCAGGCGCAGGCGNGACCGCACTANCTATGTGANGNG CTCTCNGTCGGNGNNCAGGCNATGCCCGTCATTGTCCATNTGCNGACNACCC TACTACTCTTNTGCNTGANCATGACTGCCGGGCCGANAAGTTGCGCATTGTC ACCTAACCCTGGGCGGCTGTATGTCTNCNAAAANAACTGCAAGATGCTGGGC CTGGACTACNAMCCACGGCCATCGTGTTCAAGCNCCTGGGTNTCGACGTGG AATGGCAGTTCCTCCCGTGGAANCGCTGCCTGGTGATGCTGGANCAGGGGTTG GCGTACCGNNCCCNCTACNNTTNNACCCNTCNNNAAANCNATNCCNTGCNGC TITACCCCNNCNAANCNCTNTCNGACNTGGAATTTGTGATNTTCTACNCCNA NNTANTONACONTGGNNAANAA

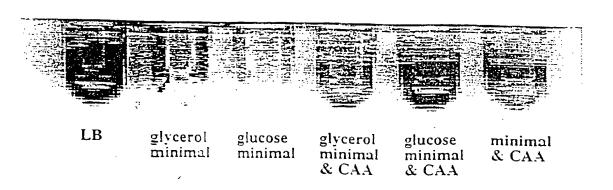


Fig. 10

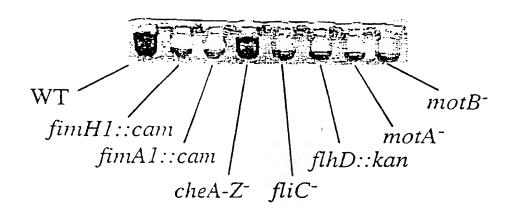
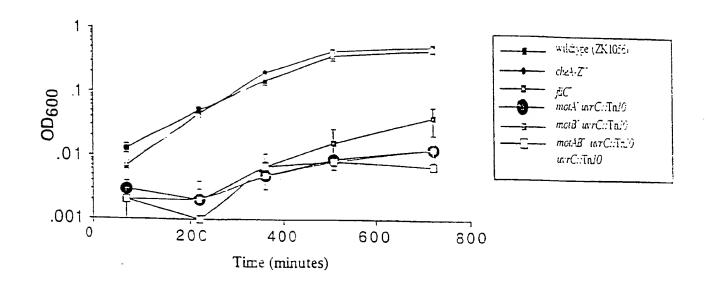


Fig. 11





WT



cheA-Z-fliC-motA-motB-motAB-

Fig. 12

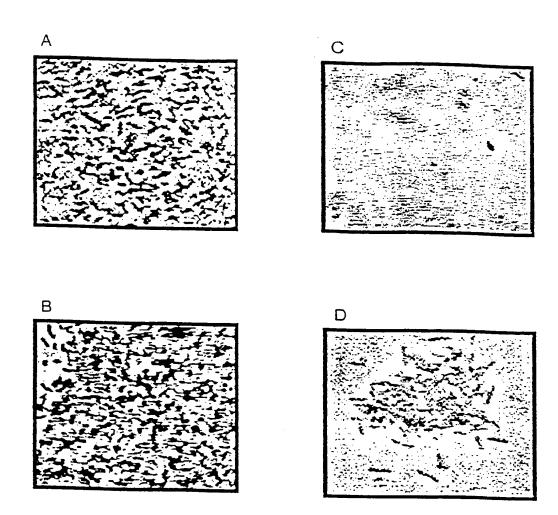


Fig. 13

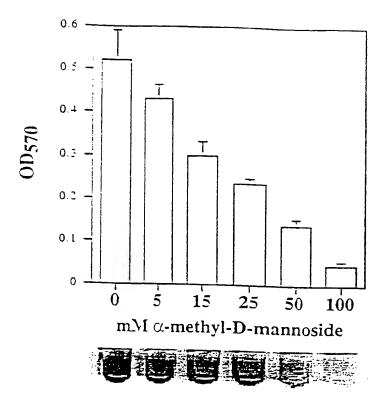


Fig. 14

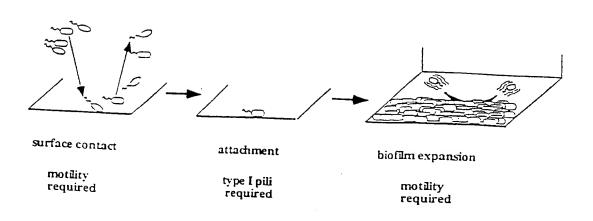


Fig. 15

wt pilY1 pilB flgK

Fig. 16

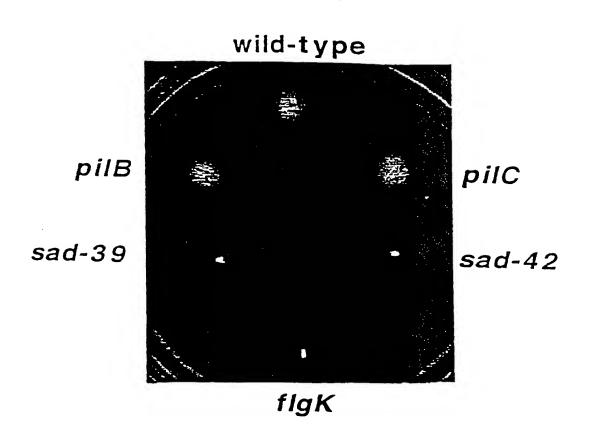


Fig. 17

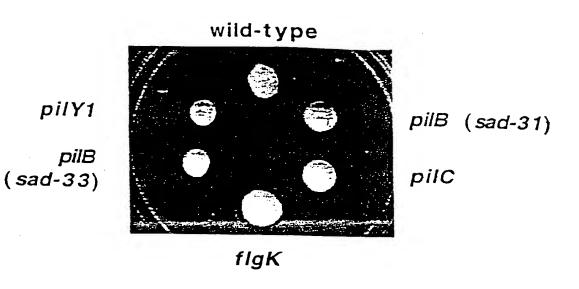


Fig. 18

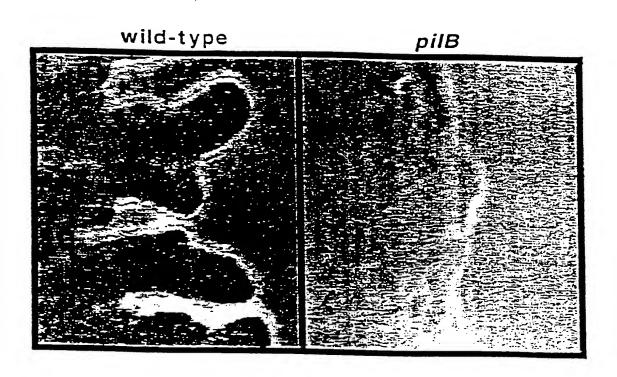


Fig.19

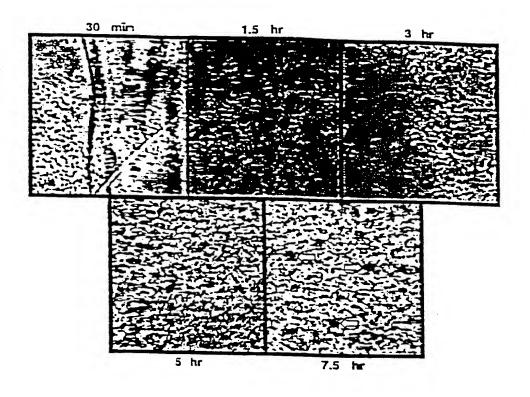


Fig. 20

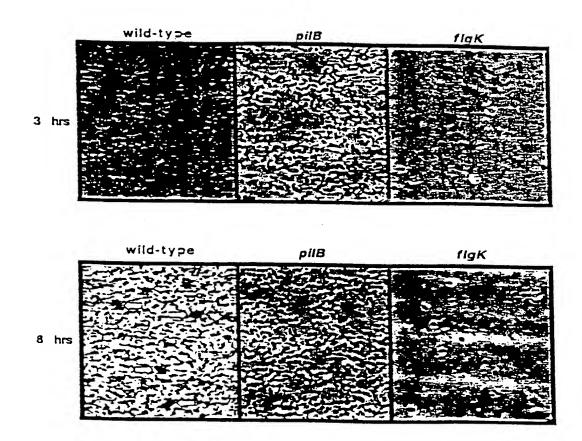


Fig. 21

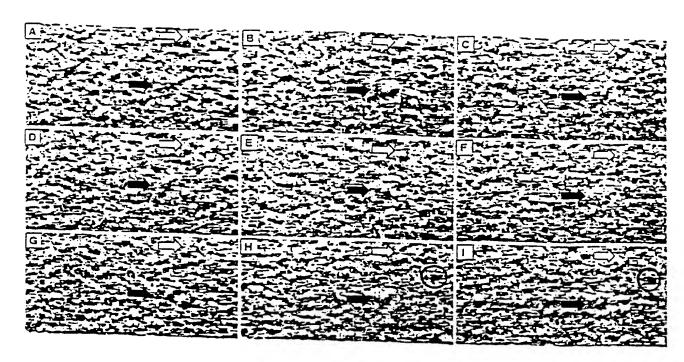


Fig. 22

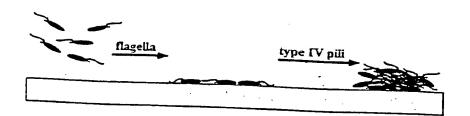


Fig. 23